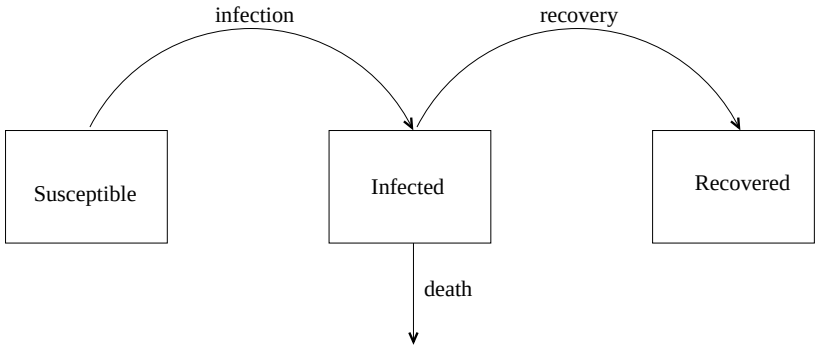
ABOUT THE LAB:

The lab will introduce the use of SimBiology, one of the Matlab-based toolboxes that allows users an easy interface to solve differential equations.

1. Simple ligand-receptor model. We will create a simple ligand-receptor model together. The model assumes that ligand binds the receptor, creating a ligand-receptor complex that is able to activate a second messenger. The ligand-receptor complex is able to unbind (to ligand and receptor) and it's also able to degrade. Save the diagram representing this system. Run the simulation with the model parameters chosen in class.

2. Modifications of our system. Assume that instead of mass-action kinetics, the second-messenger activation follows Henri-Michaelis-Menten kinetics. Explain what the biological interpretation of this mathematical assumption is. Run the simulation again (we will agree on parameters in class). How did the results of our initial simulation change?

3. SIR model
Use the diagram to simulate a basic epidemic model. Describe the assumptions of your model. Typically, people assume that the number of infections increase according to mass action kinetics, depending on both the number of susceptible and the number of infected individuals.Write down the set of differential equations that describe the SIR system. Simulate the scenario (we will agree on parameters). Initially, make the death rate (due to infections) zero. Then, slowly increase this rate. What is your observation? What does the



model predict if you allow people who have had the disease to become susceptible again?

4. Preparation for simulating stem cell fate control. Familiarize yourself with a portion of the diagram in the Mahdavi et al. article. Read the corresponding description of the paper and if necessary, look in the literature for more background. Come prepared for the next meeting (on April 5) to start implementing a diagram for your portion of the signaling cascade.